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### Title

ERRATUM: Genome-wide association study identifies loci associated with liability to alcohol and drug dependence that is associated with variability in reward-related ventral striatum activity in African- and European-Americans.

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**ERRATUM****ERRATUM: Genome-wide association study identifies loci associated with liability to alcohol and drug dependence that is associated with variability in reward-related ventral striatum activity in African- and European-Americans**

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In the original manuscript Wetherill et al., 2019 (Genes, Brain and Behavior, 18[6], July 2019, e12580), allele labels for rs1890881 were swapped during the writing, but not analyses, of the neuroimaging section. This resulted in errors which are described and corrected below. Bolded yellow highlighted sections represent errors and corrections.

†These authors made equal contributions.

1. In Table 5 on Page 11, the effect allele for rs1890881 should be labeled **C** not **T**. The beta value, including its direction of association, remains the same. The corrected table is:

**TABLE 5** Associations between response of the ventral striatum to positive > negative feedback and genotype in the Duke Neurogenetics Sample

| SNP        | Effect allele | African-Americans (AA): beta [95% C.I.], P-value |                                   | European-Americans (AA): beta [95% C.I.], P-value |                                    |
|------------|---------------|--|-----------------------------------|---|------------------------------------|
|            |               | RIGHT VS   | LEFT VS                           | RIGHT VS  | LEFT VS                            |
| rs34066662 | T             | −0.073 [−0.164-0.019],<br>0.103                  | −0.062 [−0.143-0.018],<br>0.132   | 0.002 [−0.053-0.057],<br>0.932                    | −0.008 [−0.057-0.043],<br>0.762    |
| rs75168521 | C             | −0.111 [−0.19 - −0.036],<br>0.004                | −0.065 [−0.153 - −0.24],<br>0.143 | 0.025 [−0.017-0.068],<br>0.247                    | 0.011 [−0.027-0.048],<br>0.565     |
| rs1890881  | <b>C</b>      | −0.098 [−0.175 - −0.020],<br>0.013               | −0.134 [−0.213- −0.057],<br>0.001 | −0.004 [−0.039-0.030],<br>0.801                   | −0.036 [−0.068 - −0.004],<br>0.029 |

SNP = single nucleotide polymorphism; chr5:141988181 was not available.

2.: In Results section 3.7 on Page 10, the allele label of **T** is **incorrect** in the following sentence

**ORIGINAL INCORRECT SENTENCE:** “Carriers of the minor (**T**) allele of rs1890881 (chr 1), which was associated with decreased likelihood of ANYDEP in the trans-ancestral meta-analysis (effect driven by alcohol dependence), were characterized by blunted reactivity of the left VS among AA (beta = −0.134, P = .001).”

The **corrected** sentence reads as follows:

**CORRECTED SENTENCE:** “Carriers of the minor (**C**) allele of rs1890881 (chr 1), which was associated with decreased likelihood of ANYDEP in the trans-ancestral meta-analysis (effect driven by alcohol dependence), were characterized by blunted reactivity of the left VS among AA (beta = −0.134, P = .001).”

3. In the Discussion section on page 12, the last paragraph on the left hand side begins with the following section describing the **incorrect C** allele for rs1890881

**ORIGINAL INCORRECT SENTENCE:** “In direct contrast to the results for rs75168521, rs1890881 (chromosome 1) major **C** allele homozygotes, who were at increased risk for ANYDEP (driven by the association with alcohol dependence) in the COGA GWAS, had elevated reward-related VS response (identical to Lai et al).”

The **corrected** sentences reads as follows:

**CORRECTED SENTENCE:** “In direct contrast to the results for rs75168521, rs1890881 (chromosome 1) major **T** allele homozygotes, who were at increased risk for ANYDEP (driven by the association with alcohol dependence) in the COGA GWAS, had elevated reward-related VS response (identical to Lai et al).”

Reported statistics, conclusions, and interpretations of these data remain the same. Upon re-running analyses, no other errors were identified. We apologize for any inconvenience caused to readers.

Note: The PubMed Central (PMC) version of the manuscript has been edited to incorporate these corrections.